



IFWO

RAW SEQUENCE LISTING

DATE: 08/31/2004

PATENT APPLICATION: US/10/795,933

TIME: 12:53:28

Input Set : N:\Crf3\RULE60\10795933.raw

Output Set: N:\CRF4\08312004\J795933.raw

1 <110> APPLICANT: Zavada, Jan
 2 Pastorekova, Silvia
 3 Pastorek, Jaromir
 4 <120> TITLE OF INVENTION: MN Gene and Protein
 5 <130> FILE REFERENCE: D-0021-2
 6 <140> CURRENT APPLICATION NUMBER: US/10/795,933
 7 <141> CURRENT FILING DATE: 2004-03-08
 8 <150> PRIOR APPLICATION NUMBER: US/08/260,190
 9 <151> PRIOR FILING DATE: 1994-06-15
 10 <150> PRIOR APPLICATION NUMBER: 08/177,093
 11 <151> PRIOR FILING DATE: 1993-12-30
 12 <150> PRIOR APPLICATION NUMBER: 07/964,589
 13 <151> PRIOR FILING DATE: 1992-10-21
 14 <150> PRIOR APPLICATION NUMBER: PV-709-92
 15 <151> PRIOR FILING DATE: 1992-03-11
 16 <160> NUMBER OF SEQ ID NOS: 26
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1399
 21 <212> TYPE: DNA
 22 <213> ORGANISM: HUMAN
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(1266)
 26 <400> SEQUENCE: 1
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 28 Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
 29 1 5 10 15
 30 tct ggg gaa gat gac cca ctg ggc gag gag gat ctg ccc agt gaa gag 96
 31 Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
 32 20 25 30
 33 gat tca ccc aga gag gag gat cca ccc gga gag gag gat cta cct gga 144
 34 Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
 35 35 40 45
 36 gag gag gat cta cct gga gag gag gat cta cct gaa gtt aag cct aaa 192
 37 Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
 38 50 55 60
 39 tca gaa gaa gag ggc tcc ctg aag tta gag gat cta cct act gtt gag 240
 40 Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
 41 65 70 75 80
 42 gct cct gga gat cct caa gaa ccc cag aat aat gcc cac agg gac aaa 288
 43 Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
 44 85 90 95

ENTERED

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45	gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg	336
46	Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	
47	100 105 110	
48	ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat	384
49	Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	
50	115 120 125	
51	atc cgc ccc cag ctg gcc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa	432
52	Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	
53	130 135 140	
54	ctc ctg ggc ttc cag ctg ccg ccg ctc cca gaa ctg cgc ctg cgc aac	480
55	Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	
56	145 150 155 160	
57	aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct	528
58	Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
59	165 170 175	
60	ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg cat ctg cac tgg	576
61	Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp	
62	180 185 190	
63	ggg gct gca ggt cgt ccg ggc tgc gag cac act gtg gaa ggc cac cgt	624
64	Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
65	195 200 205	
66	ttc cct gcc gag atc cac gtg gtt cac ctc agc acc gcc ttt gcc aga	672
67	Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg	
68	210 215 220	
69	gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc	720
70	Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
71	225 230 235 240	
72	ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag cag ttg ctg	768
73	Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu	
74	245 250 255	
75	tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag act cag gtc cca	816
76	Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro	
77	260 265 270	
78	gga ctg gac ata tct gca ctc ctg ccc tct gac ttc agc cgc tac ttc	864
79	Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe	
80	275 280 285	
81	caa tat gag ggg tct ctg act aca ccg ccc tgt gcc cag ggt gtc atc	912
82	Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile	
83	290 295 300	
84	tgg act gtg ttt aac cag aca gtg atg ctg agt gct aag cag ctc cac	960
85	Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His	
86	305 310 315 320	
87	acc ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg	1008
88	Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu	
89	325 330 335	
90	aac ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc	1056
91	Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser	
92	340 345 350	
93	ttc cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag	1104

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94   Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
95           355           360           365
96   ctg aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc   1152
97   Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
98       370           375           380
99   ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg   1200
100  Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
101       385           390           395           400
102  cag cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag   1248
103  Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
104           405           410           415
105  gta gcc gag act gga gcc tagaggctgg atcttgagaga atgtgagaag   1296
106  Val Ala Glu Thr Gly Ala
107           420
108  ccagccagag gcattctgagg gggagccggg aactgtcctg tcctgctcat tatgccactt 1356
109  ccttttaact gccagaagaat tttttaaaat aaatatattat aat   1399
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 422
113 <212> TYPE: PRT
114 <213> ORGANISM: HUMAN
115 <400> SEQUENCE: 2
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117      1           5           10           15
118  Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
119           20           25           30
120  Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
121           35           40           45
122  Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
123      50           55           60
124  Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
125      65           70           75           80
126  Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Ala His Arg Asp Lys
127           85           90           95
128  Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
129           100          105          110
130  Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
131           115          120          125
132  Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
133           130          135          140
134  Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
135           145          150          155          160
136  Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
137           165          170          175
138  Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
139           180          185          190
140  Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
141           195          200          205
142  Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
143           210          215          220

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144 Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
145 225 230 235 240
146 Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
147 245 250 255
148 Ser Arg Leu Glu Ile Ala Glu Gly Ser Glu Thr Gln Val Pro
149 260 265 270
150 Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
151 275 280 285
152 Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
153 290 295 300
154 Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
155 305 310 315 320
156 Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
157 325 330 335
158 Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
159 340 345 350
160 Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
161 355 360 365
162 Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly
163 370 375 380
164 Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg
165 385 390 395 400
166 Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu
167 405 410 415
168 Val Ala Glu Thr Gly Ala
169 420

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171 <210> SEQ ID NO: 3

172 <211> LENGTH: 29

173 <212> TYPE: DNA

174 <213> ORGANISM: HUMAN

175 <400> SEQUENCE: 3

176 cgcccgagtgg gtcattcttc ccagaagag

29

178 <210> SEQ ID NO: 4

179 <211> LENGTH: 19

180 <212> TYPE: DNA

181 <213> ORGANISM: HUMAN

182 <400> SEQUENCE: 4

183 ggaatcctcc tgcattccgg

19

185 <210> SEQ ID NO: 5

186 <211> LENGTH: 1522

187 <212> TYPE: DNA

188 <213> ORGANISM: HUMAN

189 <220> FEATURE:

190 <221> NAME/KEY: CDS

191 <222> LOCATION: (13)..(1389)

192 <220> FEATURE:

193 <221> NAME/KEY: mat_peptide

194 <222> LOCATION: (124)..(1389)

195 <400> SEQUENCE: 5

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196  acagtcagcc gc atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg 51
197      Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu
198      -35 -30 -25
199  atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg 99
200  Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu
201      -20 -15 -10
202  ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag 147
203  Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu
204      -5 -1 1 5
205  gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc 195
206  Asp Ser Pro Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly
207      10 15 20
208  gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca 243
209  Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro
210      25 30 35 40
211  ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag 291
212  Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu
213      45 50 55
214  gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag 339
215  Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys
216      60 65 70
217  tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc 387
218  Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro
219      75 80 85
220  cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg 435
221  Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp
222      90 95 100
223  cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg 483
224  Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala
225      105 110 115 120
226  ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc 531
227  Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe
228      125 130 135
229  tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg 579
230  Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro
231      140 145 150
232  ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc 627
233  Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr
234      155 160 165
235  ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg 675
236  Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg
237      170 175 180
238  gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg 723
239  Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser
240      185 190 195 200
241  gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt 771
242  Glu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val
243      205 210 215
244  cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg 819

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 36,37,41,42,46,47

Seq#:19; N Pos. 7

Seq#:23; N Pos. 1974,2346

Seq#:25; Xaa Pos. 3,4

Seq#:26; Xaa Pos. 3,4

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10795933.raw

Output Set: N:\CRF4\08312004\J795933.raw

L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:9
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:457 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:527 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:1920
M:341 Repeated in SeqNo=23
L:597 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:25
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:608 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0